

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 078003-0280681

In re patent application of
ADLER, JON ELLIOT et al.

Serial No. 10/035,045

Filed: January 3, 2002

For: T1R TASTE RECEPTORS AND GENES ENCODING SAME



STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and

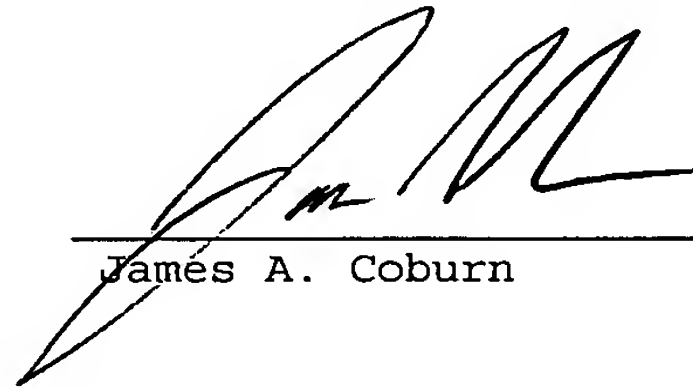
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. 10/035,045

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

March 25, 2002
Date


James A. Coburn

HARBOR CONSULTING
Intellectual Property Services
1500A Lafayette Road
Suite 262
Portsmouth, N.H.
800-318-3021



SEQUENCE LISTING

<110> ADLER, JON ELLIOT
LI, XIAODONG
STASZEWSKI, LENA
O'CONNELL, SHAWN
ZOZULYA, SERGEY

<120> T1R TASTE RECEPTORS AND GENES ENCODING SAME

<130> 078003-0280681

<140> 10/035,045

<141> 2002-01-03

<150> 60/259,227

<151> 2001-01-03

<150> 60/284,547

<151> 2001-04-19

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 876

<212> DNA

<213> Homo sapiens

<400> 1

agcctggcag	tggcctcagg	cagagtctga	cgcgcacaaa	ctttcaggcc	caggaagcga	60
ggacaccact	ggggccccag	ggtgtggcaa	gtgaggatgg	caagggtttt	gctaaacaaa	120
tcctctgccc	gctccccgcc	ccgggctcac	tccatgtgag	gccccagtcg	gggcagccac	180
ctgccgtgcc	tggttggagt	tgcctctgcc	atgctgggcc	ctgctgtcct	gggcctcagc	240
ctctgggctc	tcctgcaccc	tgggacgggg	gccccattgt	gcctgtcaca	gcaacttagg	300
atgaaggggg	actacgtgct	gggggggctg	ttccccctgg	gcgaggccga	ggaggctggc	360
ctccgcagcc	ggacacggcc	cagcagccct	gtgtgcacca	ggtacagagg	tgggacggcc	420
tgggtcgggg	tcagggtgac	caggtctggg	gtgctcctga	gctggggccg	aggtggccat	480
ctgcggttct	gtgtggcccc	aggttctcct	caaacggcct	gctctgggca	ctggccatga	540
aatggccgt	ggaggagatc	aacaacaagt	cggatctgct	gcccgggctg	cgcctgggct	600
acgacctctt	tgatacgtgc	tcggagcctg	tgggtggccat	gaagcccagc	ctcatgttcc	660
tggccaaggc	aggcagccgc	gacatcgccg	cctactgcaa	ctacacgcag	taccagcccc	720
gtgtgctggc	tgtcatcggg	ccccactcgt	cagagctcgc	catggtcacc	ggcaagttct	780
tcagcttctt	cctcatgccc	cagtggggcg	ccccccacca	tcaccacacc	ccaaccaacc	840
cctgccccgt	gggagccccct	tgtgtcagga	gaatgc			876

<210> 2

<211> 2687

<212> DNA

<213> Homo sapiens

<400> 2

tacatgcacc	ccaccagcc	ctgccctggg	agccctgtgt	cagaagatgc	tcttggcctt	60
gcaggtcagc	tacggtgcta	gcatggagct	gctgagcgcc	cgggagacct	tccccctctt	120
cttccgcacc	gtgccagcg	accgtgtgca	gctgacggcc	gccgcggagc	tgctgcagga	180
gttcggctgg	aactgggtgg	ccgccctggg	cagcgacgac	gagtacggcc	ggcagggcct	240

gagcatcttc	tcggccctgg	ccgcggcacg	cggcatctgc	atcgcgcacg	agggcctggt	300
gccgctgccc	cgtgccgatg	actcgcggt	ggggaagggtg	caggacgtcc	tgcaccaggt	360
gaaccagagc	agcgtgcagg	tgggtgctgct	gttcgcctcc	gtgcacgccg	cccacgccct	420
cttcaactac	agcatcagca	gcaggctctc	gccaagggtg	tgggtggcca	gcgaggcctg	480
gctgacctct	gacctggtca	tggggctgcc	cggcatggcc	cagatgggca	cggtgcttgg	540
cttcctccag	aggggtgccc	agctgcacga	gttccccag	tacgtgaaga	cgcacctggc	600
cctggccacc	gaccgcgcct	tctgctctgc	cctgggcgag	agggagcagg	gtctggagga	660
ggacgtgggtg	ggccagcgct	gcccgcagt	tgactgcac	acgtgcaga	acgtgagcgc	720
agggctaaat	caccaccaga	cgttctctgt	ctacgcagct	gtgtatagcg	tggcccaggc	780
cctgcacaac	actcttcagt	gcaacgcctc	aggctgcccc	gcgcaggacc	ccgtgaagcc	840
ctggcagggtg	agcccgggag	atgggggtgt	gctgtcctct	gcatgtgccc	aggccaccag	900
gcacggccac	cacgcctgag	ctggagggtg	ctggcggtc	agccccgtcc	cccgcgccga	960
gctcctggag	aacatgtaca	acctgacctt	ccacgtgggc	gggctgccgc	tgcggttcga	1020
cagcagcgga	aacgtggaca	tggagtacga	cctgaagctg	tgggtgtggc	agggtcagt	1080
gcccaggctc	cacgacgtgg	gcaggttcaa	cggcagcctc	aggacagagc	gcctgaagat	1140
ccgctggcac	acgtctgaca	accagggtgag	gtgagggtgg	gtgtgccagg	cgtgcccgtg	1200
gtagcccccg	cggcaggggc	cagcctgggg	gtggggggcc	ttccagtctc	ccgtgggcat	1260
gcccagccga	gcagagccag	accccaggcc	tgtgcgcaga	agcccgtgtc	ccggtgctcg	1320
cggcagtgcc	aggaggggcca	ggtgcgcggg	gtcaaggggg	tccactcctg	ctgctacgac	1380
tgtgtggact	gcgaggcggg	cagctaccgg	caaaaccag	gtgagccgcc	ttcccggcag	1440
gcgggggtgg	gaacgcagca	ggggagggtc	ctgccaaagt	ctgactctga	gaccagagcc	1500
cacagggtac	aagacgaaca	cccagcgccc	ttctcctctc	tcacagacga	catcgctgc	1560
accttttgtg	gccaggatga	gtggtccccg	gagcgaagca	cacgtgctt	ccgccgcagg	1620
tctcggttcc	tggcatgggg	cgagccggct	gtgctgctgc	tgtcctgct	gctgagcctg	1680
gcgctggggc	ttgtgctggc	tgtttggggg	ctgttcgttc	accatcgggg	cagcccactg	1740
gttcaggcct	cggggggggc	cctggcctgc	tttggcctgg	tgtgcctggg	cctggtctgc	1800
ctcagcgctc	tcctgttccc	tggccagccc	agccctgccc	gatgcctggc	ccagcagccc	1860
ttgtcccacc	tcccgtcac	gggctgcctg	agcacactct	tcctgcaggc	ggccgagatc	1920
ttcgtggagt	cagaactgcc	tctgagctgg	gcagaccggc	tgagtggctg	cctgcggggg	1980
ccctgggcct	ggctggtggt	gctgctggcc	atgctggtgg	aggctgcact	gtgcacctgg	2040
tacctggtgg	ccttcccgc	ggagggtggtg	acggactggc	acatgctgcc	cacggaggcg	2100
ctggtgcact	gccgcacacg	ctcctgggtc	agcttcgggc	tagcgcacgc	caccaatgcc	2160
acgtggcct	ttctctgctt	cctgggcact	ttcctggtgc	ggagccagcc	gggctgctac	2220
aaccgtgccc	gtggcctcac	ctttgccatg	ctggcctact	tcatacctg	ggtctccttt	2280
gtgcccctcc	tggccaatgt	gcaggtgggtc	ctcaggcccc	ccgtgcagat	gggcgccctc	2340
ctgctctgtg	tcctgggcat	cctggctgcc	ttccacctgc	ccagggtgta	cctgctcatg	2400
cggcagccag	ggctcaacac	ccccgagttc	ttcctgggag	ggggccctgg	ggatgcccac	2460
ggccagaatg	acgggaacac	aggaaatcag	gggaaacatg	agtgacccaa	ccctgtgatc	2520
tcagcccccg	tgaaccacga	cttagctgcg	atccccccca	agccagcaat	gaccctgtgc	2580
tcgctacaga	gaccctccc	ctctaggttc	tgaccccagg	ttgtctcctg	accctgaccc	2640
cacagtgagc	cctaggcctg	gagcacgtgg	acaccctgt	gaccatc		2687

<210> 3

<211> 2559

<212> DNA

<213> Homo sapiens

<400> 3

atgctggggc	ctgctgtcct	gggcctcagc	ctctgggctc	tcctgcaccc	tgggacgggg	60
gccccattgt	gcctgtcaca	gcaacttagg	atgaaggggg	actacgtgct	gggggggctg	120
ttccccctgg	gcgaggccga	ggaggctggc	ctccgcagcc	ggacacggcc	cagcagccct	180
gtgtgcacca	ggttctcctc	aaacggcctg	ctctggggac	tggccatgaa	aatggccgtg	240
gaggagatca	acaacaagtc	ggatctgctg	cccgggctgc	gcctgggcta	cgacctcttt	300
gatacgtgct	cggagcctgt	ggtggccatg	aagcccagcc	tcattgttct	ggccaaggca	360
ggcagccgcg	acatcgccgc	ctactgcaac	tacacgcagt	accagccccg	tgtgctggct	420
gtcatcgggc	cccactcgtc	agagctcgcc	atggtcaccg	gcaagtctct	cagcttcttc	480
ctcatgcccc	aggtcagcta	cgggtgctagc	atggagctgc	tgagcgcccc	ggagaccttc	540

```

ccttccttct tccgcaccgt gcccagcgac cgtgtgcagc tgacggccgc cgcggagctg 600
ctgcaggagt tcggctggaa ctgggtggcc gccctgggca gcgacgacga gtacggccgg 660
cagggcctga gcatcttctc ggccctggcc gcggcacgcg gcatctgcat cgcgcacgag 720
ggcctggtgc cgtgccccg tgccgatgac tcgcggtgga ggaagggtgca ggacgtcctg 780
caccaggtga accagagcag cgtgcagggt gtgctgctgt tcgcctccgt gcacgccgcc 840
cacgccctct tcaactacag catcagcagc aggtctctgc ccaagggtgtg ggtggccagc 900
gaggcctggc tgacctctga cctggtcatg gggctgcccg gcatggccca gatgggcacg 960
gtgcttggct tcctccagag ggggtgccag ctgcacgagt tccccagta cgtgaagacg 1020
cacctggccc tggccaccga cccggccttc tgctctgccc tgggcgagag ggagcagggt 1080
ctggaggagg acgtggtggg ccagcgctgc ccgcagtgtg actgcatcac gctgcagaac 1140
gtgagcgcag ggctaaatca ccaccagacg ttctctgtct acgcagctgt gtatagcgtg 1200
gcccaggccc tgcacaacac tcttcagtgc aacgcctcag gctgccccgc gcaggacccc 1260
gtgaagccct ggcagctcct ggagaacatg tacaacctga ccttccacgt gggcgggctg 1320
ccgctgcggt tcgacagcag cggaaacgtg gacatggagt acgacctgaa gctgtgggtg 1380
tggcagggtc cagtgcaccg gctccacgac gtgggcagggt tcaacggcag cctcaggaca 1440
gagcgcctga agatccgctg gcacacgtct gacaaccaga agcccgtgtc ccggtgctcg 1500
cggcagtgcc aggagggcca ggtgcgcccg gtcaagggtg tccactcctg ctgctacgac 1560
tgtgtggact gcgaggcggg cagctaccgg caaaacccag acgacatcgc ctgcaccttt 1620
tgtggccagg atgagtggc cccggagcga agcacacgct gcttccgccc caggtctcgg 1680
ttcctggcat gggcgagacc ggctgtgctg ctgctgctcc tgctgctgag cctggcgctg 1740
ggccttgtgc tggctgcttt ggggctgttc gttcaccatc gggacagccc actggttcag 1800
gcctcggggg gggccctggc ctgctttggc ctggtgtgcc tgggcctggg ctgcctcagc 1860
gtcctcctgt tccctggcca gccagccct gccgatgcc tggcccagca gcccttgtcc 1920
cacctcccgc tcacgggctg cctgagcaca ctcttctgac aggcggccga gatcttcgtg 1980
gagtcagaac tgctctgag ctgggcagac cggctgagtg gctgcctgcg ggggccctgg 2040
gcctggctgg tgggtgctgt ggccatgctg gtggaggctg cactgtgcac ctggtacctg 2100
gtggccttcc cgcggagggt ggtgacggac tggcacatgc tgcccacgga ggcgctgggt 2160
cactgccgca cacgctcctg ggtcagcttc ggcctagcgc acgccacca tgccacgctg 2220
gcctttctct gcttcttggg cactttctct gtgcggagcc agccgggctg ctacaaccgt 2280
gcccgtggcc tcacctttgc catgctggcc tacttcatca cctgggtctc ctttgtgccc 2340
ctcctggcca atgtgcagggt ggtcctcagg cccgcctgac agatgggccc cctcctgctc 2400
tgtgtcctgg gcatcctggc tgccttccac ctgcccagggt gttacctgct catgcggcag 2460
ccagggtca acacccccga gttcttctct ggagggggcc ctggggatgc ccaaggccag 2520
aatgacggga acacaggaaa tcaggggaaa catgagtga 2559

```

<210> 4

<211> 852

<212> PRT

<213> Homo sapiens

<400> 4

Met Leu Gly Pro Ala Val Leu Gly Leu Ser Leu Trp Ala Leu Leu His
1 5 10 15

Pro Gly Thr Gly Ala Pro Leu Cys Leu Ser Gln Gln Leu Arg Met Lys
20 25 30

Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
35 40 45

Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
50 55 60

Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
65 70 75 80

Glu	Glu	Ile	Asn	Asn	Lys	Ser	Asp	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly		
				85					90					95			
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Ala	Met	Lys	Pro		
			100					105					110				
Ser	Leu	Met	Phe	Leu	Ala	Lys	Ala	Gly	Ser	Arg	Asp	Ile	Ala	Ala	Tyr		
		115					120					125					
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro		
	130					135					140						
His	Ser	Ser	Glu	Leu	Ala	Met	Val	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe		
145					150					155					160		
Leu	Met	Pro	Gln	Val	Ser	Tyr	Gly	Ala	Ser	Met	Glu	Leu	Leu	Ser	Ala		
				165					170					175			
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val		
			180					185					190				
Gln	Leu	Thr	Ala	Ala	Ala	Glu	Leu	Leu	Gln	Glu	Phe	Gly	Trp	Asn	Trp		
		195					200					205					
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Glu	Tyr	Gly	Arg	Gln	Gly	Leu	Ser		
	210					215					220						
Ile	Phe	Ser	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu		
225					230					235					240		
Gly	Leu	Val	Pro	Leu	Pro	Arg	Ala	Asp	Asp	Ser	Arg	Leu	Gly	Lys	Val		
				245					250					255			
Gln	Asp	Val	Leu	His	Gln	Val	Asn	Gln	Ser	Ser	Val	Gln	Val	Val	Leu		
			260					265						270			
Leu	Phe	Ala	Ser	Val	His	Ala	Ala	His	Ala	Leu	Phe	Asn	Tyr	Ser	Ile		
		275					280					285					
Ser	Ser	Arg	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ala	Trp	Leu		
	290					295					300						
Thr	Ser	Asp	Leu	Val	Met	Gly	Leu	Pro	Gly	Met	Ala	Gln	Met	Gly	Thr		
305					310					315					320		
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Gln	Leu	His	Glu	Phe	Pro	Gln		
				325					330					335			
Tyr	Val	Lys	Thr	His	Leu	Ala	Leu	Ala	Thr	Asp	Pro	Ala	Phe	Cys	Ser		
			340					345					350				
Ala	Leu	Gly	Glu	Arg	Glu	Gln	Gly	Leu	Glu	Glu	Asp	Val	Val	Gly	Gln		
		355					360					365					
Arg	Cys	Pro	Gln	Cys	Asp	Cys	Ile	Thr	Leu	Gln	Asn	Val	Ser	Ala	Gly		
	370					375					380						

Leu	Asn	His	His	Gln	Thr	Phe	Ser	Val	Tyr	Ala	Ala	Val	Tyr	Ser	Val	385	390	395	400
Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln	Cys	Asn	Ala	Ser	Gly	Cys	Pro	405	410	415	
Ala	Gln	Asp	Pro	Val	Lys	Pro	Trp	Gln	Leu	Leu	Glu	Asn	Met	Tyr	Asn	420	425	430	
Leu	Thr	Phe	His	Val	Gly	Gly	Leu	Pro	Leu	Arg	Phe	Asp	Ser	Ser	Gly	435	440	445	
Asn	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys	Leu	Trp	Val	Trp	Gln	Gly	Ser	450	455	460	
Val	Pro	Arg	Leu	His	Asp	Val	Gly	Arg	Phe	Asn	Gly	Ser	Leu	Arg	Thr	465	470	475	480
Glu	Arg	Leu	Lys	Ile	Arg	Trp	His	Thr	Ser	Asp	Asn	Gln	Lys	Pro	Val	485	490	495	
Ser	Arg	Cys	Ser	Arg	Gln	Cys	Gln	Glu	Gly	Gln	Val	Arg	Arg	Val	Lys	500	505	510	
Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	Cys	Glu	Ala	Gly	Ser	515	520	525	
Tyr	Arg	Gln	Asn	Pro	Asp	Asp	Ile	Ala	Cys	Thr	Phe	Cys	Gly	Gln	Asp	530	535	540	
Glu	Trp	Ser	Pro	Glu	Arg	Ser	Thr	Arg	Cys	Phe	Arg	Arg	Arg	Ser	Arg	545	550	555	560
Phe	Leu	Ala	Trp	Gly	Glu	Pro	Ala	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu	565	570	575	
Ser	Leu	Ala	Leu	Gly	Leu	Val	Leu	Ala	Ala	Leu	Gly	Leu	Phe	Val	His	580	585	590	
His	Arg	Asp	Ser	Pro	Leu	Val	Gln	Ala	Ser	Gly	Gly	Pro	Leu	Ala	Cys	595	600	605	
Phe	Gly	Leu	Val	Cys	Leu	Gly	Leu	Val	Cys	Leu	Ser	Val	Leu	Leu	Phe	610	615	620	
Pro	Gly	Gln	Pro	Ser	Pro	Ala	Arg	Cys	Leu	Ala	Gln	Gln	Pro	Leu	Ser	625	630	635	640
His	Leu	Pro	Leu	Thr	Gly	Cys	Leu	Ser	Thr	Leu	Phe	Leu	Gln	Ala	Ala	645	650	655	
Glu	Ile	Phe	Val	Glu	Ser	Glu	Leu	Pro	Leu	Ser	Trp	Ala	Asp	Arg	Leu	660	665	670	
Ser	Gly	Cys	Leu	Arg	Gly	Pro	Trp	Ala	Trp	Leu	Val	Val	Leu	Leu	Ala	675	680	685	

Met Leu Val Glu Val Ala Leu Cys Thr Trp Tyr Leu Val Ala Phe Pro
 690 695 700
 Pro Glu Val Val Thr Asp Trp His Met Leu Pro Thr Glu Ala Leu Val
 705 710 715 720
 His Cys Arg Thr Arg Ser Trp Val Ser Phe Gly Leu Ala His Ala Thr
 725 730 735
 Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu Gly Thr Phe Leu Val Arg
 740 745 750
 Ser Gln Pro Gly Cys Tyr Asn Arg Ala Arg Gly Leu Thr Phe Ala Met
 755 760 765
 Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val Pro Leu Leu Ala Asn
 770 775 780
 Val Gln Val Val Leu Arg Pro Ala Val Gln Met Gly Ala Leu Leu Leu
 785 790 795 800
 Cys Val Leu Gly Ile Leu Ala Ala Phe His Leu Pro Arg Cys Tyr Leu
 805 810 815
 Leu Met Arg Gln Pro Gly Leu Asn Thr Pro Glu Phe Phe Leu Gly Gly
 820 825 830
 Gly Pro Gly Asp Ala Gln Gly Gln Asn Asp Gly Asn Thr Gly Asn Gln
 835 840 845
 Gly Lys His Glu
 850

<210> 5
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (3)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (9)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (12)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (18)
 <223> a, t, c, g, other or unknown

<400> 5
 cgnttyytng cntggggnga rcc

23

<210> 6
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (3)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (6)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (18)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (21)
 <223> a, t, c, g, other or unknown

<400> 6
 cgngcncgrt trtarcanc ngg

23

<210> 7
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 7
 Arg Phe Leu Ala Trp Gly Glu Pro Ala
 1 5

<210> 8
 <211> 8
 <212> PRT
 <213> Homo sapiens

<400> 8

Pro Gly Cys Tyr Asn Arg Ala Arg

1

5

<210> 9

<211> 552

<212> DNA

<213> Mus sp.

<400> 9

```

gtgctgtcac tcctcctgct gctttgcctg gtgctgggtc tagcactggc tgctctgggg 60
ctctctgtcc accactggga cagccctctt gtccaggcct caggcggtc acagttctgc 120
tttggcctga tctgcctagg cctcttctgc ctcagtgtcc ttctgttccc aggacggcca 180
agctctgcca gctgccttgc acaacaacca atggctcacc tccctctcac aggctgcctg 240
agcacactct tcctgcaagc agctgagacc tttgtggagt ctgagctgcc actgagctgg 300
gcaaactggc tatgcagcta ccttcgggac tctggcctgc tagtgggtact gttggccact 360
tttgtggagg cagcactatg tgcttgggat ttgaccgctt caccagaagt ggtgacagac 420
tggtcagtgc tgcccacaga ggtactggag cactgccacg tgcgttcctg ggtcaacctg 480
ggcttggtgc acatcaccaa tgcaatggta gcttttctct gctttctggg cactttcctg 540
gtacaagacc ag                                     552

```

<210> 10

<211> 184

<212> PRT

<213> Mus sp.

<400> 10

```

Val Leu Ser Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu
 1                      5                      10                      15

Ala Ala Leu Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln
                20                      25                      30

Ala Ser Gly Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu
    35                      40                      45

Phe Cys Leu Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser
    50                      55                      60

Cys Leu Ala Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu
    65                      70                      75                      80

Ser Thr Leu Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu
                85                      90                      95

Pro Leu Ser Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Asp Ser Gly
    100                      105                      110

Leu Leu Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala
    115                      120                      125

Trp Tyr Leu Thr Ala Ser Pro Glu Val Val Thr Asp Trp Ser Val Leu
    130                      135                      140

Pro Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Asn Leu
    145                      150                      155                      160

```

Gly Leu Val His Ile Thr Asn Ala Met Val Ala Phe Leu Cys Phe Leu
 165 170 175

Gly Thr Phe Leu Val Gln Asp Gln
 180

<210> 11
 <211> 558
 <212> DNA
 <213> Rattus sp.

<400> 11
 gtgctgtcac ttctcctgct gctttgectg gtgctgggcc tgacactggc tgccctgggg 60
 ctctttgtcc actactggga cagccctctt gttcaggcct caggtgggtc actgttctgc 120
 tttggcctga tctgcctagg cctcttctgc ctcagtgtcc ttctgttccc aggacgacca 180
 cgctctgcca gctgccttgc ccaacaacca atggctcacc tccctctcac aggctgcctg 240
 agcacactct tcctgcaagc agccgagatc tttgtggagt ctgagctgcc actgagttgg 300
 gcaaactggc tctgcagcta ccttcggggc ccctgggctt ggctgggtgg actgctggcc 360
 actcttgtgg aggctgcact atgtgcctgg tacttgatgg ctttccctcc agaggtggtg 420
 acagattggc aggtgctgcc cacggaggta ctggaacact gccgcatgcg ttcctgggtc 480
 agcctgggct tgggtgcacat caccaatgca ggggtagctt tcctctgctt tctgggcact 540
 ttcttggtac aaagccag 558

<210> 12
 <211> 186
 <212> PRT
 <213> Rattus sp.

<400> 12
 Val Leu Ser Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu
 1 5 10 15
 Ala Ala Leu Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln
 20 25 30
 Ala Ser Gly Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu
 35 40 45
 Phe Cys Leu Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser
 50 55 60
 Cys Leu Ala Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu
 65 70 75 80
 Ser Thr Leu Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu
 85 90 95
 Pro Leu Ser Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp
 100 105 110
 Ala Trp Leu Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys
 115 120 125
 Ala Trp Tyr Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln
 130 135 140

Val Leu Pro Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val
145 150 155 160

Ser Leu Gly Leu Val His Ile Thr Asn Ala Gly Val Ala Phe Leu Cys
165 170 175

Phe Leu Gly Thr Phe Leu Val Gln Ser Gln
180 185

<210> 13

<211> 2577

<212> DNA

<213> Rattus sp.

<400> 13

```

atgccggggtt tggctatctt gggcctcagt ctggctgctt tcctggagct tgggatgggg 60
tcctctttgt gtctgtcaca gcaattcaag gcacaagggg actatatatt ggggtggacta 120
tttcccctgg gcacaactga ggaggccact ctcaaccaga gaacacagcc caacggcatc 180
ctatgtacca ggttctcgcc ccttggtttg ttctggcca tggctatgaa gatggctgta 240
gaggagatca acaatggatc tgccttgctc cctgggctgc gactgggcta tgacctgttt 300
gacacatgct cagagccagt ggtcaccatg aagcccagcc tcatgttcat ggccaagggtg 360
ggaagtcaaa gcattgctgc ctactgcaac tacacacagt accaaccctg tgtgctggct 420
gtcattgggtc cccactcatc agagcttgcc ctcattacag gcaagttctt cagcttcttc 480
ctcatgccac aggtcagcta tagtgccagc atggatcggc taagtgaccg ggaaacattt 540
ccatccttct tccgcacagt gccagtgac cgggtgcagc tgcaggccgt tgtgacactg 600
ttgcagaatt tcagctggaa ctgggtggct gccttaggta gtgatgatga ctatggcccg 660
gaaggtctga gcactctttc tgggtctggcc aactcacgag gtatctgcat tgcacacgag 720
ggcctgggtgc cacaacatga cactagtggc caacaattgg gcaaggtggg ggatgtgcta 780
cgccaagtga accaaagcaa agtacagggtg gtgggtgctgt ttgcatctgc ccgtgctgtc 840
tactcccttt ttagctacag catccttcat gacctctcac ccaaggatat ggtggccagt 900
gagtcctggc tgacctctga cctgggtcatg acacttccca atattgcccg tgtgggcact 960
gttcttgggt ttctgcagcg cgggtgccct ctgcctgaat tttcccatta tgtggagact 1020
cgccttgccc tagctgctga cccaacattc tgtgcctccc tgaaagctga gttggatctg 1080
gaggagcgcg tgatggggcc acgctgttca caatgtgact acatcatgct acagaacctg 1140
tcacttgggc tgatgcagaa cctatcagct gggcagttgc accaccaa atttgcaacc 1200
tatgcagctg tgtacagtgt ggctcaggcc cttcacaaca ccctgcagtg caatgtctca 1260
cattgccaca catcagagcc tgttcaacct tggcagctcc tggagaacat gtacaatatg 1320
agtttccgtg ctcgagactt gacactgcag ttgatgcca aaggagtggt agacatggaa 1380
tatgacctga agatgtgggt gtggcagagc cctacacctg tactacatac tgtaggcacc 1440
ttcaacggca cccttcagct gcagcactcg aaaatgtatt ggccaggcaa ccagggtgcca 1500
gtctcccagt gctcccggca gtgcaaagat ggccagggtg gcagagtaaa gggctttcat 1560
tcctgctgct atgactgtgt ggactgcaag gcagggagct accggaagca tccagatgac 1620
ttcacctgta ctccatgtgg caaggatcag tgggtccccag aaaaaagcac aacctgctta 1680
cctcgcaggc ccaagtttct ggcttggggg gagccagctg tgetgtcact tctcctgctg 1740
ctttgcctgg tgctgggcct gacactggct gccctggggc tctttgtcca ctactgggac 1800
agccctcttg ttcaggcctc aggtgggtca ctgttctgct ttggcctgat ctgcctaggc 1860
ctcttctgcc tcagtgtcct tctgttccca ggacgaccac gctctgccag ctgccttgcc 1920
caacaaccaa tggctcacct ccctctcaca ggctgcctga gcacactctt cctgcaagca 1980
gccgagatct ttgtggagtc tgagctgcca ctgagttggg caaactggct ctgcagctac 2040
cttcggggcc cctgggcttg gctgggtgga ctgctggcca ctcttggtga ggctgcacta 2100
tgtgcctggt acttgatggc ttccctcca gaggtgggtga cagattggca ggtgctgccc 2160
acggaggtag tggaaactg ccgcatgcgt tcctgggtca gcctgggctt ggtgcacatc 2220
accaatgcag tgttagcttt cctctgcttt ctgggcactt tcctgggtaca gagccagcct 2280
ggctcgtata accgtgcccg tggcctcacc ttcgccatgc tagcttattt catcatctgg 2340
gtctcttttg tgccctcct ggctaagtgt caggtggcct accagccagc tgtgcagatg 2400
ggtgctatct tattctgtgc cctgggcatc ctggccacct tccacctgcc caaatgctat 2460

```

gtactttctgt ggctgccaga gctcaacacc caggagttct tcctgggaag gagccccaag 2520
 gaagcatcag atgggaatag tggtagtagt gaggcaactc ggggacacag tgaatga 2577

<210> 14
 <211> 858
 <212> PRT
 <213> Rattus sp.

<400> 14
 Met Pro Gly Leu Ala Ile Leu Gly Leu Ser Leu Ala Ala Phe Leu Glu
 1 5 10 15
 Leu Gly Met Gly Ser Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
 20 25 30
 Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Thr Thr Glu Glu
 35 40 45
 Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Gly Ile Leu Cys Thr Arg
 50 55 60
 Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
 65 70 75 80
 Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
 85 90 95
 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Pro
 100 105 110
 Ser Leu Met Phe Met Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
 115 120 125
 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
 130 135 140
 His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
 145 150 155 160
 Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
 165 170 175
 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
 180 185 190
 Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
 195 200 205
 Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser
 210 215 220
 Ile Phe Ser Gly Leu Ala Asn Ser Arg Gly Ile Cys Ile Ala His Glu
 225 230 235 240
 Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
 245 250 255

Val	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val			
			260					265					270					
Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile			
		275					280					285						
Leu	His	Asp	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu			
	290					295					300							
Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr			
305					310					315					320			
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His			
				325					330					335				
Tyr	Val	Glu	Thr	Arg	Leu	Ala	Leu	Ala	Ala	Asp	Pro	Thr	Phe	Cys	Ala			
			340					345					350					
Ser	Leu	Lys	Ala	Glu	Leu	Asp	Leu	Glu	Glu	Arg	Val	Met	Gly	Pro	Arg			
		355					360					365						
Cys	Ser	Gln	Cys	Asp	Tyr	Ile	Met	Leu	Gln	Asn	Leu	Ser	Ser	Gly	Leu			
	370					375					380							
Met	Gln	Asn	Leu	Ser	Ala	Gly	Gln	Leu	His	His	Gln	Ile	Phe	Ala	Thr			
385					390					395					400			
Tyr	Ala	Ala	Val	Tyr	Ser	Val	Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln			
				405					410					415				
Cys	Asn	Val	Ser	His	Cys	His	Thr	Ser	Glu	Pro	Val	Gln	Pro	Trp	Gln			
			420					425					430					
Leu	Leu	Glu	Asn	Met	Tyr	Asn	Met	Ser	Phe	Arg	Ala	Arg	Asp	Leu	Thr			
		435					440					445						
Leu	Gln	Phe	Asp	Ala	Lys	Gly	Ser	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys			
	450					455					460							
Met	Trp	Val	Trp	Gln	Ser	Pro	Thr	Pro	Val	Leu	His	Thr	Val	Gly	Thr			
465					470					475					480			
Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	His	Ser	Lys	Met	Tyr	Trp	Pro	Gly			
				485					490					495				
Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln			
			500					505					510					
Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp			
			515				520					525						
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr			
	530					535					540							
Pro	Cys	Gly	Lys	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Thr	Cys	Leu			
545					550					555					560			

Pro	Arg	Arg	Pro	Lys	Phe	Leu	Ala	Trp	Gly	Glu	Pro	Ala	Val	Leu	Ser	565	570	575	
Leu	Leu	Leu	Leu	Leu	Cys	Leu	Val	Leu	Gly	Leu	Thr	Leu	Ala	Ala	Leu	580	585	590	
Gly	Leu	Phe	Val	His	Tyr	Trp	Asp	Ser	Pro	Leu	Val	Gln	Ala	Ser	Gly	595	600	605	
Gly	Ser	Leu	Phe	Cys	Phe	Gly	Leu	Ile	Cys	Leu	Gly	Leu	Phe	Cys	Leu	610	615	620	
Ser	Val	Leu	Leu	Phe	Pro	Gly	Arg	Pro	Arg	Ser	Ala	Ser	Cys	Leu	Ala	625	630	635	640
Gln	Gln	Pro	Met	Ala	His	Leu	Pro	Leu	Thr	Gly	Cys	Leu	Ser	Thr	Leu	645	650	655	
Phe	Leu	Gln	Ala	Ala	Glu	Ile	Phe	Val	Glu	Ser	Glu	Leu	Pro	Leu	Ser	660	665	670	
Trp	Ala	Asn	Trp	Leu	Cys	Ser	Tyr	Leu	Arg	Gly	Pro	Trp	Ala	Trp	Leu	675	680	685	
Val	Val	Leu	Leu	Ala	Thr	Leu	Val	Glu	Ala	Ala	Leu	Cys	Ala	Trp	Tyr	690	695	700	
Leu	Met	Ala	Phe	Pro	Pro	Glu	Val	Val	Thr	Asp	Trp	Gln	Val	Leu	Pro	705	710	715	720
Thr	Glu	Val	Leu	Glu	His	Cys	Arg	Met	Arg	Ser	Trp	Val	Ser	Leu	Gly	725	730	735	
Leu	Val	His	Ile	Thr	Asn	Ala	Val	Leu	Ala	Phe	Leu	Cys	Phe	Leu	Gly	740	745	750	
Thr	Phe	Leu	Val	Gln	Ser	Gln	Pro	Gly	Arg	Tyr	Asn	Arg	Ala	Arg	Gly	755	760	765	
Leu	Thr	Phe	Ala	Met	Leu	Ala	Tyr	Phe	Ile	Ile	Trp	Val	Ser	Phe	Val	770	775	780	
Pro	Leu	Leu	Ala	Asn	Val	Gln	Val	Ala	Tyr	Gln	Pro	Ala	Val	Gln	Met	785	790	795	800
Gly	Ala	Ile	Leu	Phe	Cys	Ala	Leu	Gly	Ile	Leu	Ala	Thr	Phe	His	Leu	805	810	815	
Pro	Lys	Cys	Tyr	Val	Leu	Leu	Trp	Leu	Pro	Glu	Leu	Asn	Thr	Gln	Glu	820	825	830	
Phe	Phe	Leu	Gly	Arg	Ser	Pro	Lys	Glu	Ala	Ser	Asp	Gly	Asn	Ser	Gly	835	840	845	
Ser	Ser	Glu	Ala	Thr	Arg	Gly	His	Ser	Glu							850	855		

<210> 15
 <211> 8194
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1251)..(1300)
 <223> a, t, c, g, other or unknown

<220>
 <221> modified_base
 <222> (1951)..(2000)
 <223> a, t, c, g, other or unknown

<400> 15
 gagaatctcg cgagatcccc tcggtccgcc ccgctgccct cccagctgcc gaaaagaggg 60
 gcctccgagc cgccggcgcc ctctgccggc aacctccgga agcacactag gaggttccag 120
 ccgatctggt cgaggggctc cacggaggac tccatttacg ttacgcaa at tccctacccc 180
 agccggccgg agagagaaag ccagaaacct cgcgaccagc catggggccac ctctccggaa 240
 aaacaccggg atattttttt tctcctgcag aaaaagcttt aggattggca gtttaaaca 300
 aacatgtcta tttgcatacc ttcggtttgc atgcatttgt ttcgaagtga gcaaccctgg 360
 gtaacaaggc gaaagtatat gacaatttgc tcagaatctt aatgtcagaa aactggagac 420
 tggggcaggg ggggtgtcgac tcaaagctgt gtctcattta gtaaactgag gccaggtaa 480
 aaagtcttga aacctcgcaa caccgggaga aattgtgttc cagcctccca cctcgcccca 540
 aaatgccaga gctccttttc taagccaggc gaagtcacag agcgtggaca gaaccacaa 600
 ccgtccagag gaagggtcac tgggtgccac ctggtttgca tctgtgcctt cgtcctgccc 660
 agttcctgag tgggaccgca ggcccggaat gtcaaggcaa acagtcctgc ttcagccact 720
 gggctccagt cccacccctt ttggggggcct gaagttagga agcatccggc agctgccttc 780
 tatttaagca actggcctcc ttagaggcca ctcttgccc atgccaggcg cgggcatctg 840
 gccagcatgc tgctctgcac ggctcgccctg gtccggcctgc agcttctcat ttcctgctgc 900
 tggggcctttg cctgccatag cacggagtct tctcctgact tcaccctccc cggagattac 960
 ctctggcag gcctgttccc tctccattct ggctgtctgc aggtgaggca cagacccgag 1020
 gtgaccctgt gtgacagggt agtgaggggc cagcagagcc acacttagtg ggacccctgg 1080
 ctatagggcc cctctggctg ccacccctcca aacaggacct tgcctctgcc tttgcccctt 1140
 gaactgtccc caggccttgt tcatcaatcc acttgccacc taagtgtctg ctagaccttc 1200
 ctagacactt cggccagttt ccaattatct cacccttgct gttagaatgt nnnnnnnnnn 1260
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn aattccttaa actaaatttc 1320
 tcactttctc tctctctctg gaaaacactg actaatgtag caggtttctc tgctccagga 1380
 cttcaggacc ttttcgatgc taataagtct ctccatcagg gccagcttgt tctcctact 1440
 gagcttgaga gcccttggtg aagttgtggt ttgggggact ggaccgatga cctcaaaggc 1500
 tccctttgct cccaagcctc agagtctagg aggccagagg gtctcagcag gcctttgtcc 1560
 ttctcagctg tctcttactg gctttctcca caggctctgt agcttcaatg agcatggcta 1620
 ccacctcttc caggctatgc ggcttggggg tgaggagata aacaactcca cggccctgct 1680
 gcccacatc accctggggg accagctgta tgatgtgtgt tctgactctg ccaatgtgta 1740
 tgccacgctg agagtgtctt ccctgccagg gcaacaccac atagagctcc aaggagacct 1800
 tctccactat tcccctacgg tgctggcagt gattgggcct gacagacca accgtgctgc 1860
 caccacagcc gccctgctga gccctttcct ggtgcccctg gtaagctgga gcctcagacc 1920
 tttgcccctc tcccttcagg caagtctggg nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1980
 nnnnnnnnnn nnnnnnnnnn gccaccatgc cgggctaatt tttttgtatt tttagtagag 2040
 acgggggttc accgtgttag ccaggctggt cgaaaactcc taacctcgtg atccaccac 2100
 ctccggcctc caatgtgctg ggattacagg tgtgagccac tgcaccgggc cataatgtat 2160
 taatataata aaataattat acaactcacc ataattgtag atcagtggga gccctgagct 2220
 tgttttccta caactagatg gtcccatctg ggggtgatgg gagacagtga cagatcatca 2280
 gacattagat tctcataagt agcgtgcaac ccagatccct cgcattgtga gttcacagta 2340
 gggttcaagc tctacaaga atctgatgct gctgctgac tgacaggagg ggagcagctg 2400
 taaatacaga tgaagcttcg cttactcacc agctgctcac ctctcctgt gagggccggc 2460
 tcctaacagg ccactgacct aacttctgcc ctgacctaca catgcttctc ttcttccttg 2520

caaactgcct	ccagtggaag	tccctgaagg	tccccaaaca	cacgggacta	tttcactcct	2580
atgcagggtt	tgtctccttt	gcttggaatg	catccccctca	ccccttggtc	ccaggcagat	2640
tcccacccct	cccccagaac	ctgccccagt	ggagccttcg	cagggtgattt	gtcagtttca	2700
caggctgagg	ggtgctctcc	tggtctcccc	ggctccctgt	atccccacac	ccagcacagg	2760
gccaggcact	gggggggcct	tcagtggaga	ctgaaatggc	tgaacgggac	ctcccataga	2820
ttagctatgc	ggccagcagc	gagacgctca	gcgtgaagcg	gcagtatccc	tctttcctgc	2880
gcaccatccc	caatgacaag	taccagggtg	agaccatggt	gctgctgctg	cagaagttcg	2940
ggtggacctg	gatctctctg	gttggcagca	gtgacgacta	tgggcagcta	ggggtgcagg	3000
cactggagaa	ccaggccact	ggtcagggga	tctgcattgc	tttcaaggac	atcatgccct	3060
tctctgcccc	ggtgggcgat	gagaggatgc	agtgcctcat	gcgccacctg	gcccaggccg	3120
gggccaccgt	cgtggttgtt	ttttccagcc	ggcagttggc	cagggtgttt	ttcgagtccg	3180
tggtgctgac	caacctgact	ggcaagggtg	gggtcgccctc	agaagcctgg	gccctctcca	3240
ggcacatcac	tggggtgccc	gggatccagc	gcattgggat	ggtgctgggc	gtggccatcc	3300
agaagagggc	tgtccctggc	ctgaaggcgt	ttgaagaagc	ctatgcccg	gcagacaaga	3360
aggccccctag	gccttgccac	aagggtcctc	ggtgcagcag	caatcagctc	tgcagagaa	3420
gccaagcttt	catggcacac	acgatgcccc	agctcaaagc	cttctccatg	agttctgcct	3480
acaacgcata	ccgggctgtg	tatgcggtgg	cccatggcct	ccaccagctc	ctgggctgtg	3540
cctctggagc	ttgttccagg	ggccgagtct	acccctggca	ggtaagagag	cccaccccag	3600
cacctcctgt	cagggagaa	agccaatcct	gagatgagca	gagtgggcac	tctccggtca	3660
ctctaaatgc	caagggggat	aaatgccact	aacttgaggt	tttttgtttt	gttttgtttt	3720
gttttttgag	acagtctggc	tctgtcacc	aggctgcagt	gtagtgatgc	gatctcggct	3780
ctctgcaact	tccacctcct	gggttcaagt	gattctcttg	cctcggcctc	ctgagtagct	3840
gggattacag	gcaccacca	ccatgcctgg	ataatttttc	ttttcttttt	tttttttttg	3900
agatagagtc	tcgctctgtt	gcccaggctg	gaatgcagtg	gtgcgatctt	ggctcactgt	3960
gagctccgcc	tcccagggtc	actccattcc	cctgcctcag	cctcccaagt	aggtgggact	4020
acgggcgccc	gccaccacgc	ccagctaatt	ttttttgtat	tttgagtaga	gacgggggtt	4080
caccatgtta	gccaggatgg	tctcaatctc	ctgaccttgt	catccgcccc	cctcgtcctc	4140
ccaaagtgct	gggattacag	gcgtgagcca	ccgcaccccg	cctaattttt	gtatttttag	4200
tagagatggg	gtttcaccat	gttggccagg	ctggtctcga	actcctggca	tcaagtgate	4260
ctcctgcttc	ggcctcccaa	agtgtctggg	ttacaggcat	tagctctctt	ctcttagaca	4320
gatctttctc	tctgactcct	gccttctctc	accactgtg	tcttggaagt	gtcaagtgat	4380
aagatccagg	gctaaaactg	tctgtaaaagg	agtgtttgtt	agaggcctcc	tctcaggagg	4440
ttggtgggga	agattgaggg	gcttcctaag	aaggaaggga	cgagaccttc	ctgatgggct	4500
gaaaccacca	ggacggaaac	ccaggaaggc	cccaggccct	tgcttctggg	accatgtggg	4560
tctgtgctgt	ctgtgggtgg	ttcatgatac	gcgtttcttt	cagcttttgg	agcagatcca	4620
caaggtgcat	tcccttctac	acaaggacac	tgtggcggtt	aatgacaaca	gagatcccct	4680
cagtagctat	aacataattg	cctgggactg	gaatggaccc	aagtggacct	tcacggtcct	4740
cggttcctcc	acatgggtctc	cagttcagct	aaacataaat	gagacaaaaa	tccagtggca	4800
cggaaaggac	aaccaggtaa	tggggatgtg	gctactcacc	atgtaactgg	cttatgggca	4860
acctagagcc	tgggggtgat	gctgacacag	tgtacaggga	gcaggagggg	ggccccagg	4920
gtccagctgc	caccactcta	cccatacctg	ccagggaagc	agggaagaca	ctccgtaggc	4980
gagtgtgcag	atgccctggg	gcggaagtcc	acacgaccag	gggccctgcc	ctgggagtga	5040
gccctgaggg	cagatgcaca	gagattctgt	tttctgttcc	acatgtgagc	tgtcctttga	5100
cttgggcccc	tacgtgtggc	ccctctggct	tcttacagg	gcctaagtct	gtgtgttcca	5160
gcgactgtct	tgaagggcac	cagcgagtgg	ttacgggttt	ccatcactgc	tgctttgagt	5220
gtgtgccctg	tggggctggg	accttccctc	acaagagtgg	tgagtgggca	atggagcagg	5280
cgagctaccc	agcactccc	ggggctgcac	ggtggaggga	gggcctccct	tgggccccat	5340
gtgccctgcc	ccagaaccaa	ggcccagtc	ctgggctgcc	agttagcttc	agggtggagg	5400
acacctgcta	ccagacagaa	ttctgatcaa	gagaatcagc	cactgggtgc	ggtggctcat	5460
gcctgtaatc	ccagcacttt	gggaggctga	ggcgggtgga	tcacttgagg	tcgggagttc	5520
gagaccagcc	tggccaacat	ggtgaaaccc	catctctacc	aaaaatataa	aaaattagct	5580
gggtgtgggtg	gcgcgtgcct	gtaatcccag	ctactcggga	ggctgaggca	ggagaatcac	5640
ttgaaccag	gaggcggagg	ttgcagtga	ccaagatgca	ttccagcctg	gaccacaaag	5700
cgagaattcg	tccccccaaa	aaaagaaagg	aggccggg	cggtggctca	cacctgtaat	5760
cccagcactt	tgggaggccg	agggtgggtg	atcacctgag	gtcaggagtt	cgagaccagc	5820
ctgaccaaca	tgggtgaaacc	ccatctctac	taaaaataca	aaaaaagtta	gccgggcgtt	5880
gtggcgtgtg	cctgtaattc	cagctactcg	ggaggctgag	gcaggagaa	tgcttgaacc	5940
cgggaggcgg	agggtgcagt	gagccaagat	tgcaccattg	cactccagcc	tgggcgacaa	6000

gagaaaaact	ctgtctcaaa	aaaaaagaaa	gaaagaaaga	attagccaac	tgaaagcctt	6060
agactgaggt	gtgtcctctg	ttagagagct	gtcatcacaa	ctcctacaaa	agcagtcgta	6120
tcctgaattc	aacctctttc	tctaaatgaa	tatagctatt	gttccctttg	tgccctcttg	6180
tcctactgtc	ccttctgttg	cccatgccaa	agacagctag	ctccttgaac	agcttggcct	6240
gaatacagat	actagcgtgt	ctgcagcaga	gaaaaaaaca	gcattcccca	tccagaaatg	6300
caaggtcaag	aacagagagc	aaattaggta	gctaaggact	caggtcctta	gttgggtgtcc	6360
agggggccaca	ttctttcctt	tcaccatctc	tgtagggaca	ggaatacttc	ccttctgtcc	6420
tcagaggggtc	aggactcaga	gaaaccacag	agcagcagct	caggaaagtg	gttcatggaa	6480
atgctggcaa	gagagagggg	ttacaatgcc	ctcccttggg	agcaggctgc	tcccatcaga	6540
tcgtaacctc	tctgggtatgt	gggcagagct	accagggttaa	ggtcctccct	agggtttgca	6600
aaacctcat	gggatcatga	gccatacaga	accgacctgt	gtgtctccag	agtctgtaat	6660
taacacaggc	atthttgagga	aatgcgtggc	ctcaggcccc	actcccggct	acccccatcc	6720
cactatgcct	agtatagtct	agctgccctg	gtacaattct	cccagtatct	tgaggcccc	6780
tatttcctat	tcctactctg	ctcatctggc	tctcaggaac	cttcttggcc	ttccctttca	6840
gacctctaca	gatgccagcc	ttgtgggaaa	gaagagtggg	cacctgaggg	aagccagacc	6900
tgcttcccgc	gcactgtggg	gttttttggc	ttgcgtgagc	acacctcttg	gggtgctgctg	6960
gcagctaaca	cgctgctgct	gctgctgctg	cttgggactg	ctggcctgtt	tgcttggcac	7020
ctagacaccc	ctgtgggtgag	gtcagcaggg	ggccgcctgt	gctttcttat	gctgggctcc	7080
ctggcagcag	gtagtggcag	cctctatggc	ttctttgggg	aaccacaaag	gcctgcgtgc	7140
ttgctacgcc	aggccctctt	tgcccttggg	ttcaccatct	tcctgtcctg	cctgacagtt	7200
cgctcattcc	aactaatcat	catcttcaag	ttttccacca	aggtacctac	attctaccac	7260
gcctgggtcc	aaaaccacgg	tgctggcctg	tttgtgatga	tcagctcagc	ggcccagctg	7320
cttatctgtc	taacttggct	gggtggtgtg	acccactgc	ctgctaggga	ataccagcgc	7380
ttcccccatc	tggtgatgct	tgagtgcaca	gagaccaact	ccctgggctt	catactggcc	7440
ttcctctaca	atggcctcct	ctccatcagt	gcctttgcct	gcagctacct	gggtaaggac	7500
ttgccagaga	actacaacga	ggccaaatgt	gtcaccttca	gcctgctctt	caacttcgtg	7560
tcctggatcg	ccttcttcac	cacggccagc	gtctacgacg	gcaagtacct	gcctgcggcc	7620
aacatgatgg	ctgggctgag	cagcctgagc	agcggcttcg	gtgggtatth	tctgcctaag	7680
tgctacgtga	tcctctgccg	cccagacctc	aacagcacag	agcacttcca	ggcctccatt	7740
caggactaca	cgaggcgctg	cggctccacc	tgaccagtgg	gtcagcaggc	acggctggca	7800
gccttctctg	ccctgagggg	cgaaggctga	gcaggccggg	gggtgtccggg	aggtcttttg	7860
gcatcgcggt	ctgggggttg	gacgtgtaag	cgcctgggag	agcctagacc	aggctccggg	7920
ctgccaataa	agaagtgaag	tgcgatatctg	gtctcctgtc	gtgggagagt	gtgaggtgta	7980
acggattcaa	gtctgaaccc	agagcctgga	aaaggctgac	cgcccagatt	gacgttgcta	8040
ggcaactccg	gaggcggggc	cagcgccaaa	agaacagggc	gaggcgctcg	ccccgcattc	8100
cattggccgt	tctctgcggg	gccccgcctt	cgggggcccg	agctagaagc	tctacgcttc	8160
cgaggcgcac	ctcctggcct	gcacgctttg	acgt			8194

<210> 16

<211> 2526

<212> DNA

<213> Homo sapiens

<400> 16

atgctgctct	gcacggctcg	cctggctggc	ctgcagcttc	tcatttcctg	ctgctgggccc	60
tttgccctgcc	atagcacgga	gtcttctcct	gacttcaccc	tccccggaga	ttacctcctg	120
gcaggcctgt	tccctctcca	ttctggctgt	ctgcagggtga	ggcacagacc	cgagggtgacc	180
ctgtgtgaca	ggctctttag	cttcaatgag	catggctacc	acctcttcca	ggctatgcgg	240
cttgggggttg	aggagataaa	caactccacg	gcctgctgc	ccaacatcac	cctgggggtac	300
cagctgtatg	atgtgtgttc	tgactctgcc	aatgtgtatg	ccacgctgag	agtgtctctcc	360
ctgccagggc	aacaccacat	agagctccaa	ggagaccttc	tccactattc	ccctacgggtg	420
ctggcagtgga	ttgggcctga	cagcaccaac	cgtgctgcca	ccacagccgc	cctgctgagc	480
cctttcctgg	tgcccatgat	tagctatgcg	gccagcagcg	agacgctcag	cgtgaagcgg	540
cagtatccct	ctttcctgcg	caccatcccc	aatgacaagt	accagggtgga	gaccatgggtg	600
ctgctgctgc	agaagtccgg	gtggacctgg	atctctctgg	ttggcagcag	tgacgactat	660
gggcagctag	gggtgcaggc	actggagaa	caggccactg	gtcaggggat	ctgcattgct	720
ttcaaggaca	tcatgccctt	ctctgcccag	gtgggcgatg	agaggatgca	gtgcctcatg	780

```

cgccacctgg cccaggccgg ggccaccgtc gtggttggtt tttccagccg gcagttggcc 840
aggggtgttt tcgagtccgt ggtgctgacc aacctgactg gcaaggtgtg ggtcgcctca 900
gaagcctggg ccctctccag gcacatcact ggggtgcccc ggatccagcg cattgggatg 960
gtgctgggcg tggccatcca gaagagggct gtccctggcc tgaaggcgtt tgaagaagcc 1020
tatgcccggg cagacaagaa ggcccctagg ccttgccaca agggctcctg gtgcagcagc 1080
aatcagctct gcagagaatg ccaagctttc atggcacaca cgatgcccaa gctcaaagcc 1140
ttctccatga gttctgccta caacgcatac cgggctgtgt atgcggtggc ccatggcctc 1200
caccagctcc tgggctgtgc ctctggagct tgttccaggg gccgagtcta cccctggcag 1260
cttttgagag agatccacaa ggtgcatttc cttctacaca aggacactgt ggcgtttaat 1320
gacaacagag atcccctcag tagctataac ataattgcct gggactggaa tggacccaag 1380
tggaccttca cggtcctcgg ttcctccaca tgggtctccag ttcagctaaa cataaatgag 1440
acaaaaatcc agtggcacgg aaaggacaac caggtgccta agtctgtgtg ttccagcgac 1500
tgtcttgaag ggcaccagcg agtgggttacg ggtttccatc actgctgctt tgagtgtgtg 1560
ccctgtgggg ctgggacctt cctcaacaag agtgacctct acagatgcca gccttgtggg 1620
aaagaagagt gggcacctga ggggaagccag acctgcttcc cgcgcaactgt ggtgtttttg 1680
gctttgcgtg agcacacctc ttgggtgctg ctggcagcta acacgctgct gctgctgctg 1740
ctgcttggga ctgctggcct gtttgccctg cacctagaca cccctgtggg gaggtcagca 1800
gggggcccgc tgtgctttct tatgctgggc tccctggcag caggtagtgg cagcctctat 1860
ggcttctttg gggaaaccac aaggcctgcg tgcttgctac gccaggccct ctttgccctt 1920
ggtttcacca tcttctgtc ctgcctgaca gttcgctcat tccaactaat catcatcttc 1980
aagttttcca ccaaggtacc tacattctac cacgcctggg tccaaaacca cgggtgctggc 2040
ctgtttgtga tgatcagctc agcggcccag ctgcttatct gtctaacttg gctggtggtg 2100
tggacccac tgctgctag ggaataccag cgcttcccc atctggtgat gcttgagtgc 2160
acagagacca actccctggg cttcatactg gccttccctt acaatggcct cctctccatc 2220
agtgcctttg cctgcagcta cctgggtaag gacttgccag agaactacaa cgaggccaaa 2280
tgtgtcacct tcagcctgct cttcaacttc gtgtcctgga tcgccttctt caccacggcc 2340
agcgtctacg acggcaagta cctgcctgcg gccaacatga tggctgggct gagcagcctg 2400
agcagcggct tcggtgggta ttttctgcct aagtgtctag tgatcctctg ccgcccagac 2460
ctcaacagca cagagcactt ccaggcctcc attcaggact acacgaggcg ctgcggctcc 2520
acctga 2526

```

<210> 17

<211> 841

<212> PRT

<213> Homo sapiens

<400> 17

```

Met Leu Leu Cys Thr Ala Arg Leu Val Gly Leu Gln Leu Leu Ile Ser
 1              5              10              15

Cys Cys Trp Ala Phe Ala Cys His Ser Thr Glu Ser Ser Pro Asp Phe
      20              25              30

Thr Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
      35              40              45

Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
      50              55              60

Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg
      65              70              75              80

Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile
      85              90              95

Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val
      100             105             110

```

Tyr	Ala	Thr	Leu	Arg	Val	Leu	Ser	Leu	Pro	Gly	Gln	His	His	Ile	Glu
	115						120					125			
Leu	Gln	Gly	Asp	Leu	Leu	His	Tyr	Ser	Pro	Thr	Val	Leu	Ala	Val	Ile
	130					135					140				
Gly	Pro	Asp	Ser	Thr	Asn	Arg	Ala	Ala	Thr	Thr	Ala	Ala	Leu	Leu	Ser
145					150					155					160
Pro	Phe	Leu	Val	Pro	Met	Ile	Ser	Tyr	Ala	Ala	Ser	Ser	Glu	Thr	Leu
				165					170					175	
Ser	Val	Lys	Arg	Gln	Tyr	Pro	Ser	Phe	Leu	Arg	Thr	Ile	Pro	Asn	Asp
			180					185					190		
Lys	Tyr	Gln	Val	Glu	Thr	Met	Val	Leu	Leu	Leu	Gln	Lys	Phe	Gly	Trp
		195					200					205			
Thr	Trp	Ile	Ser	Leu	Val	Gly	Ser	Ser	Asp	Asp	Tyr	Gly	Gln	Leu	Gly
	210					215					220				
Val	Gln	Ala	Leu	Glu	Asn	Gln	Ala	Thr	Gly	Gln	Gly	Ile	Cys	Ile	Ala
225					230					235					240
Phe	Lys	Asp	Ile	Met	Pro	Phe	Ser	Ala	Gln	Val	Gly	Asp	Glu	Arg	Met
				245					250					255	
Gln	Cys	Leu	Met	Arg	His	Leu	Ala	Gln	Ala	Gly	Ala	Thr	Val	Val	Val
			260					265					270		
Val	Phe	Ser	Ser	Arg	Gln	Leu	Ala	Arg	Val	Phe	Phe	Glu	Ser	Val	Val
		275					280					285			
Leu	Thr	Asn	Leu	Thr	Gly	Lys	Val	Trp	Val	Ala	Ser	Glu	Ala	Trp	Ala
	290					295					300				
Leu	Ser	Arg	His	Ile	Thr	Gly	Val	Pro	Gly	Ile	Gln	Arg	Ile	Gly	Met
305					310					315					320
Val	Leu	Gly	Val	Ala	Ile	Gln	Lys	Arg	Ala	Val	Pro	Gly	Leu	Lys	Ala
				325					330					335	
Phe	Glu	Glu	Ala	Tyr	Ala	Arg	Ala	Asp	Lys	Lys	Ala	Pro	Arg	Pro	Cys
			340					345					350		
His	Lys	Gly	Ser	Trp	Cys	Ser	Ser	Asn	Gln	Leu	Cys	Arg	Glu	Cys	Gln
		355					360					365			
Ala	Phe	Met	Ala	His	Thr	Met	Pro	Lys	Leu	Lys	Ala	Phe	Ser	Met	Ser
		370				375					380				
Ser	Ala	Tyr	Asn	Ala	Tyr	Arg	Ala	Val	Tyr	Ala	Val	Ala	His	Gly	Leu
385					390					395					400
His	Gln	Leu	Leu	Gly	Cys	Ala	Ser	Gly	Ala	Cys	Ser	Arg	Gly	Arg	Val
				405					410					415	

Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu
 420 425 430
 His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser
 435 440 445
 Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr
 450 455 460
 Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu
 465 470 475 480
 Thr Lys Ile Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val
 485 490 495
 Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe
 500 505 510
 His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu
 515 520 525
 Asn Lys Ser Asp Leu Tyr Arg Cys Gln Pro Cys Gly Lys Glu Glu Trp
 530 535 540
 Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu
 545 550 555 560
 Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu
 565 570 575
 Leu Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu
 580 585 590
 Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met
 595 600 605
 Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly
 610 615 620
 Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu
 625 630 635 640
 Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu
 645 650 655
 Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala
 660 665 670
 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala
 675 680 685
 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu
 690 695 700
 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys
 705 710 715 720

Thr	Glu	Thr	Asn	Ser	Leu	Gly	Phe	Ile	Leu	Ala	Phe	Leu	Tyr	Asn	Gly
				725					730					735	
Leu	Leu	Ser	Ile	Ser	Ala	Phe	Ala	Cys	Ser	Tyr	Leu	Gly	Lys	Asp	Leu
			740					745					750		
Pro	Glu	Asn	Tyr	Asn	Glu	Ala	Lys	Cys	Val	Thr	Phe	Ser	Leu	Leu	Phe
		755					760					765			
Asn	Phe	Val	Ser	Trp	Ile	Ala	Phe	Phe	Thr	Thr	Ala	Ser	Val	Tyr	Asp
	770					775					780				
Gly	Lys	Tyr	Leu	Pro	Ala	Ala	Asn	Met	Met	Ala	Gly	Leu	Ser	Ser	Leu
785					790					795					800
Ser	Ser	Gly	Phe	Gly	Gly	Tyr	Phe	Leu	Pro	Lys	Cys	Tyr	Val	Ile	Leu
			805					810						815	
Cys	Arg	Pro	Asp	Leu	Asn	Ser	Thr	Glu	His	Phe	Gln	Ala	Ser	Ile	Gln
			820					825					830		
Asp	Tyr	Thr	Arg	Arg	Cys	Gly	Ser	Thr							
	835						840								

<210> 18

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

<220>

<221> MOD_RES

<222> (1)

<223> Thr or Arg

<220>

<221> MOD_RES

<222> (3)

<223> Phe or Leu

<220>

<221> MOD_RES

<222> (4)

<223> Arg, Gln or Pro

<220>

<221> MOD_RES

<222> (6)

<223> Arg or Thr

<220>

<221> MOD_RES

<222> (7)

<223> Ser, Pro or Val

<220>
 <221> MOD_RES
 <222> (8)
 <223> Val, Glu, Arg, Lys or Thr

<220>
 <221> MOD_RES
 <222> (11)
 <223> Ala or Glu

<220>
 <221> MOD_RES
 <222> (12)
 <223> Trp or Leu

<220>
 <221> MOD_RES
 <222> (13)
 <223> Arg, His or Gly

<400> 18
 Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu
 1 5 10

<210> 19
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<220>
 <221> MOD_RES
 <222> (1)
 <223> Leu or Gln

<220>
 <221> MOD_RES
 <222> (3)
 <223> Glu, Gly or Thr

<220>
 <221> MOD_RES
 <222> (4)
 <223> Asn, Arg or Cys

<220>
 <221> MOD_RES
 <222> (7)
 <223> Arg or Glu

<220>
 <221> MOD_RES
 <222> (9)

<223> Arg or Lys

<220>

<221> MOD_RES

<222> (10)

<223> Cys, Gly or Phe

<220>

<221> MOD_RES

<222> (11)

<223> Val, Leu or Ile

<220>

<221> MOD_RES

<222> (13)

<223> Phe or Leu

<220>

<221> MOD_RES

<222> (14)

<223> Ala or Ser

<220>

<221> MOD_RES

<222> (15)

<223> Met or Leu

<400> 19

Xaa	Pro	Xaa	Xaa	Tyr	Asn	Xaa	Ala	Xaa	Xaa	Xaa	Thr	Xaa	Xaa	Xaa
1				5				10						15

<210> 20

<211> 3563

<212> DNA

<213> Homo sapiens

<400> 20

agcctggcag	tggcctcagg	cagagtctga	cgcgcacaaa	ctttcaggcc	caggaagcga	60
ggacaccact	ggggccccag	ggtgtggcaa	gtgaggatgg	caagggtttt	gctaaacaaa	120
tcctctgccc	gctccccgcc	ccgggctcac	tccatgtgag	gccccagtcg	gggcagccac	180
ctgccgtgcc	tgttggaagt	tgcctctgcc	atgctggggc	ctgctgtcct	gggcctcagc	240
ctctgggctc	tcctgcaccc	tgggacgggg	gccccattgt	gcctgtcaca	gcaacttagg	300
atgaaggggg	actacgtgct	gggggggctg	ttccccctgg	gcgaggccga	ggaggctggc	360
ctccgcagcc	ggacacggcc	cagcagccct	gtgtgcacca	ggtacagagg	tgggacggcc	420
tgggtcgggg	tcagggtgac	caggtctggg	gtgctcctga	gctggggccg	aggtggccat	480
ctgcggttct	gtgtggcccc	aggttctcct	caaacggcct	gctctgggca	ctggccatga	540
aatggccgt	ggaggagatc	aacaacaagt	cggatctgct	gcccgggctg	cgcctgggct	600
acgacctctt	tgatacgtgc	tcggagcctg	tgggtggccat	gaagcccagc	ctcatgttcc	660
tggccaaggc	aggcagccgc	gacatcgccg	cctactgcaa	ctacacgcag	taccagcccc	720
gtgtgctggc	tgtcatcggg	ccccactcgt	cagagctcgc	catggtcacc	ggcaagttct	780
tcagcttctt	cctcatgccc	cagtggggcg	ccccccacca	tcacccaccc	ccaaccaacc	840
cctgccccgt	gggagcccct	tgtgtcagga	gaatgctaca	tgcacccac	ccagccctgc	900
cctgggagcc	ctgtgtcaga	agatgctctt	ggccttgtag	gtcagctacg	gtgctagcat	960
ggagctgctg	agcgcccggg	agaccttccc	ctccttcttc	cgcaccgtgc	ccagcgaccg	1020
tgtgcagctg	acggccgccc	cggagctgct	gcaggagttc	ggctggaact	gggtggccgc	1080
cctgggcagc	gacgacgagt	acggccggca	gggcctgagc	atcttctcgg	ccctggccgc	1140
ggcacgcggc	atctgcatcg	cgcacgaggg	cctggtgccg	ctgccccgtg	ccgatgactc	1200


```

gcggtctggg aaggtgcagg acgtcctgca ccaggtgaac cagagcagcg tgcaggtggt 1260
gctgctgttc gcctccgtgc acgccgcccc cgcctctctc aactacagca tcagcagcag 1320
gctctcgccc aaggtgtggg tggccagcga ggcctggctg acctctgacc tggatcatggg 1380
gctgcccggc atggcccaga tgggcacggg gcttggtctc ctccagaggg gtgcccagct 1440
gcacgagttc cccagtagc tgaagacgca cctggccctg gccaccgacc cggccttctg 1500
ctctgccctg ggcgagaggg agcaggggtct ggaggaggac gtggtgggccc agcgctgccc 1560
gcagtgtgac tgcatacgc tgcagaacgt gagcgagagg ctaaatacacc accagacgtt 1620
ctctgtctac gcagctgtgt atagcgtggc ccaggccctg cacaacactc ttcagtgcga 1680
cgctcaggc tgccccgcgc aggaccccggt gaagccctgg caggtgagcc cgggagatgg 1740
gggtgtgctg tcctctgcat gtgcccaggc caccaggcac ggccaccacg cctgagctgg 1800
aggtggctgg cggctcagcc ccgtcccccg cccgcagctc ctggagaaca tgtacaacct 1860
gaccttccac gtggggcggg tgccgctgct gtctgacagc agcggaacac tggacatgga 1920
gtacgacctg aagctgtggg tgtggcaggg ctcatgccc aggtccacg acgtgggcag 1980
gttcaacggc agcctcagga cagagcgct gaagatccgc tggcacacgt ctgacaacca 2040
ggtgaggtga ggggtgggtgt gccaggcgtg cccgtggtag ccccccgcggc agggcgagc 2100
ctgggggtgg gggccgttcc agtctcccggt gggcatgccc agccgagcag agccagacct 2160
caggcctgtg cgcagaagcc cgtgtcccggt tgctcgccgc agtgccagga gggccaggtg 2220
cgccgggtca aggggttcca ctctgtctgc tacgactgtg tggactgcga ggcgggcagc 2280
taccggcaaa acccaggtga gccgccttcc cggcaggcgg ggggtgggaac gcagcagggg 2340
agggctcctg caagtcctga ctctgagacc agagcccaca ggggtacaaga cgaacaccca 2400
gcgcccttct cctctctcac agacgacatc gcctgcacct tttgtggcca ggatgagtgg 2460
tccccggagc gaagcacacg ctgcttccgc cgcaggctct ggttccctggc atggggcgag 2520
ccggctgtgc tgctgctgct cctgctgctg agcctggcgc tgggccttgt gctggctgct 2580
ttggggctgt tcgttcacca tcgggacagc ccactggttc aggcctcggg ggggcccctg 2640
gcctgctttg gcctgggtgt cctgggcctg gtctgcctca gcgtcctcct gttccctggc 2700
cagcccagcc ctgcccgatg cctggcccag cagcccttgt cccacctccc gctcacgggc 2760
tgctgagca cactcttct gcaggcggcc gagatcttcg tggagtcaga actgcctctg 2820
agctgggcag accggtgag tggtgcctg cgggggcccct gggcctggct ggtggtgctg 2880
ctggccatgc tgggtggaggt cgcactgtgc acctggtacc tgggtggcctt cccgccggag 2940
gtggtgacgg actggcacat gctgcccacg gaggcgctgg tgcactgccg cacacgctcc 3000
tgggtcagct tcggcctagc gcacgccacc aatgccacgc tggcctttct ctgcttctg 3060
ggcactttcc tgggtgcggag ccagccgggc tgctacaacc gtgcccgtgg cctcaccttt 3120
gccatgctgg cctacttcat cacctgggtc tcctttgtgc ccctcctggc caatgtgcag 3180
gtggtcctca ggcccgcgt gcagatgggc gccctcctgc tctgtgtcct gggcatcctg 3240
gctgccttcc acctgcccag gtgttacctg ctcatgcggc agccagggtt caacaccccc 3300
gagttcttcc tgggaggggg ccctggggat gcccaaggcc agaatacagg gaacacagga 3360
aatcagggga aacatgagtg acccaaccct gtgatctcag ccccggtgaa cccagactta 3420
gctgcgatcc ccccaagcc agcaatgacc cgtgtctcgc tacagagacc ctcccgctct 3480
aggttctgac cccaggttgt ctctgaccc tgaccccaca gtgagcccta ggcctggagc 3540
acgtggacac ccctgtgacc atc 3563

```

<210> 21

<211> 839

<212> PRT

<213> Homo sapiens

<400> 21

```

Met Gly Pro Arg Ala Lys Thr Ile Cys Ser Leu Phe Phe Leu Leu Trp
  1                      5                      10                      15

```

```

Val Leu Ala Glu Pro Ala Glu Asn Ser Asp Phe Tyr Leu Pro Gly Asp
      20                      25                      30

```

```

Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
      35                      40                      45

```

Val	His	Leu	Asn	Phe	Leu	Gln	Val	Pro	Met	Cys	Lys	Glu	Tyr	Glu	Val
50						55					60				
Lys	Val	Ile	Gly	Tyr	Asn	Leu	Met	Gln	Ala	Met	Arg	Phe	Ala	Val	Glu
65					70					75					80
Glu	Ile	Asn	Asn	Asp	Ser	Ser	Leu	Leu	Pro	Gly	Val	Leu	Leu	Gly	Tyr
				85					90					95	
Glu	Ile	Val	Asp	Val	Cys	Tyr	Ile	Ser	Asn	Asn	Val	Gln	Pro	Val	Leu
			100					105					110		
Tyr	Phe	Leu	Ala	His	Glu	Asp	Asn	Leu	Leu	Pro	Ile	Gln	Glu	Asp	Tyr
		115					120					125			
Ser	Asn	Tyr	Ile	Ser	Arg	Val	Val	Ala	Val	Ile	Gly	Pro	Asp	Asn	Ser
						135					140				
Glu	Ser	Val	Met	Thr	Val	Ala	Asn	Phe	Leu	Ser	Leu	Phe	Leu	Leu	Pro
145					150					155					160
Gln	Ile	Thr	Tyr	Ser	Ala	Ile	Ser	Asp	Glu	Leu	Arg	Asp	Lys	Val	Arg
				165					170					175	
Phe	Pro	Ala	Leu	Leu	Arg	Thr	Thr	Pro	Ser	Ala	Asp	His	His	Val	Glu
			180					185					190		
Ala	Met	Val	Gln	Leu	Met	Leu	His	Phe	Arg	Trp	Asn	Trp	Ile	Ile	Val
		195					200					205			
Leu	Val	Ser	Ser	Asp	Thr	Tyr	Gly	Arg	Asp	Asn	Gly	Gln	Leu	Leu	Gly
		210				215					220				
Glu	Arg	Val	Ala	Arg	Arg	Asp	Ile	Cys	Ile	Ala	Phe	Gln	Glu	Thr	Leu
225					230					235					240
Pro	Thr	Leu	Gln	Pro	Asn	Gln	Asn	Met	Thr	Ser	Glu	Glu	Arg	Gln	Arg
				245					250					255	
Leu	Val	Thr	Ile	Val	Asp	Lys	Leu	Gln	Gln	Ser	Thr	Ala	Arg	Val	Val
			260					265					270		
Val	Val	Phe	Ser	Pro	Asp	Leu	Thr	Leu	Tyr	His	Phe	Phe	Asn	Glu	Val
		275					280					285			
Leu	Arg	Gln	Asn	Phe	Thr	Gly	Ala	Val	Trp	Ile	Ala	Ser	Glu	Ser	Trp
		290				295					300				
Ala	Ile	Asp	Pro	Val	Leu	His	Asn	Leu	Thr	Glu	Leu	Gly	His	Leu	Gly
305					310					315					320
Thr	Phe	Leu	Gly	Ile	Thr	Ile	Gln	Ser	Val	Pro	Ile	Pro	Gly	Phe	Ser
				325				330					335		
Glu	Phe	Arg	Glu	Trp	Gly	Pro	Gln	Ala	Gly	Pro	Pro	Pro	Leu	Ser	Arg
			340					345					350		

Thr	Ser	Gln	Ser	Tyr	Thr	Cys	Asn	Gln	Glu	Cys	Asp	Asn	Cys	Leu	Asn	
		355					360					365				
Ala	Thr	Leu	Ser	Phe	Asn	Thr	Ile	Leu	Arg	Leu	Ser	Gly	Glu	Arg	Val	
		370					375					380				
Val	Tyr	Ser	Val	Tyr	Ser	Ala	Val	Tyr	Ala	Val	Ala	His	Ala	Leu	His	
385							390					395			400	
Ser	Leu	Leu	Gly	Cys	Asp	Lys	Ser	Thr	Cys	Thr	Lys	Arg	Val	Val	Tyr	
		405								410				415		
Pro	Trp	Gln	Leu	Leu	Glu	Glu	Ile	Trp	Lys	Val	Asn	Phe	Thr	Leu	Leu	
		420					425					430				
Asp	His	Gln	Ile	Phe	Phe	Asp	Pro	Gln	Gly	Asp	Val	Ala	Leu	His	Leu	
		435					440					445				
Glu	Ile	Val	Gln	Trp	Gln	Trp	Asp	Arg	Ser	Gln	Asn	Pro	Phe	Gln	Ser	
450							455					460				
Val	Ala	Ser	Tyr	Tyr	Pro	Leu	Gln	Arg	Gln	Leu	Lys	Asn	Ile	Gln	Asp	
465							470					475			480	
Ile	Ser	Trp	His	Thr	Val	Asn	Asn	Thr	Ile	Pro	Met	Ser	Met	Cys	Ser	
		485								490				495		
Lys	Arg	Cys	Gln	Ser	Gly	Gln	Lys	Lys	Lys	Pro	Val	Gly	Ile	His	Val	
		500					505					510				
Cys	Cys	Phe	Glu	Cys	Ile	Asp	Cys	Leu	Pro	Gly	Thr	Phe	Leu	Asn	His	
		515					520					525				
Thr	Glu	Asp	Glu	Tyr	Glu	Cys	Gln	Ala	Cys	Pro	Asn	Asn	Glu	Trp	Ser	
530							535					540				
Tyr	Gln	Ser	Glu	Thr	Ser	Cys	Phe	Lys	Arg	Gln	Leu	Val	Phe	Leu	Glu	
545					550					555			560			
Trp	His	Glu	Ala	Pro	Thr	Ile	Ala	Val	Ala	Leu	Leu	Ala	Ala	Leu	Gly	
		565					570					575				
Phe	Leu	Ser	Thr	Leu	Ala	Ile	Leu	Val	Ile	Phe	Trp	Arg	His	Phe	Gln	
		580					585					590				
Thr	Pro	Ile	Val	Arg	Ser	Ala	Gly	Gly	Pro	Met	Cys	Phe	Leu	Met	Leu	
		595					600					605				
Thr	Leu	Leu	Leu	Val	Ala	Tyr	Met	Val	Val	Pro	Val	Tyr	Val	Gly	Pro	
610							615					620				
Pro	Lys	Val	Ser	Thr	Cys	Leu	Cys	Arg	Gln	Ala	Leu	Phe	Pro	Leu	Cys	
625					630					635			640			
Phe	Thr	Ile	Cys	Ile	Ser	Cys	Ile	Ala	Val	Arg	Ser	Phe	Gln	Ile	Val	
		645					650					655				

Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp
 660 665 670
 Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu
 675 680 685
 Lys Met Val Ile Val Val Ile Gly Met Leu Ala Thr Gly Leu Ser Pro
 690 695 700
 Thr Thr Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys
 705 710 715 720
 Asn Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu
 725 730 735
 Leu Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu
 740 745 750
 Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe
 755 760 765
 Tyr Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser
 770 775 780
 Gly Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu
 785 790 795 800
 Leu Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu
 805 810 815
 Phe Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln
 820 825 830
 Gly Tyr Thr Met Arg Arg Asp
 835

<210> 22

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
PDZIP peptide sequence

<400> 22

Ser Val Ser Thr Val Val
1 5

<210> 23

<211> 2520

<212> DNA

<213> Homo sapiens

<400> 23

atggggccca gggcaaagac catctgctcc ctgttcttcc tcctatgggt cctggctgag 60

```

cgggctgaga actcggactt ctacctgcct ggggattacc tcctgggtgg cctcttctcc 120
ctccatgcca acatgaaggg cattgttcac cttaacttcc tgcaggtgcc catgtgcaag 180
gagtatgaag tgaaggtgat aggctacaac ctcatgcagg ccatgcgctt cgcggtggag 240
gagatcaaca atgacagcag cctgctgcct ggtgtgctgc tgggctatga gatcgtggat 300
gtgtgctaca tctccaacaa tgtccagccg gtgctctact tcctggcaca cgaggacaac 360
ctccttccca tccaagagga ctacagtaac tacatttccc gtgtgggtggc tgtcattggc 420
cctgacaact ccgagtctgt catgactgtg gccaaacttcc tctccctatt tctccttcca 480
cagatcacct acagcgccat cagcgatgag ctgcgagaca aggtgcgctt cccggctttg 540
ctgcgtagca caccagcgc cgaccaccac gtcgaggcca tgggtgcagct gatgctgcac 600
ttccgctgga actggatcat tgtgctggtg agcagcgaca cctatggccg cgacaatggc 660
cagctgcttg gcgagcgcgt ggcccggcgc gacatctgca tcgccttcca ggagacgctg 720
cccacactgc agcccaacca gaacatgacg tcagaggagc gccagcgctt ggtgaccatt 780
gtggacaagc tgcagcagag cacagcgcgc gtcgtggtcg tgttctcgcc cgacctgacc 840
ctgtaccact tcttcaatga ggtgctgcgc cagaacttca cgggcgcctg gtggatcgcc 900
tccgagtcct gggccatcga cccggtcctg cacaacctca cggagctggg ccacttgggc 960
accttctctg gcataccat ccagagcgtg cccatcccgg gcttcagtga gttccgcgag 1020
tggggcccac aggtctgggc gccaccctc agcaggacca gccagagcta tacctgcaac 1080
caggagtgcg acaactgcct gaacgccacc ttgtccttca acaccattct caggctctct 1140
ggggagcgtg tcgtctacag cgtgtactct gcggtctatg ctgtggccca tgccctgcac 1200
agcctcctcg gctgtgacaa aagcacctgc accaagaggg tgggtctacc ctggcagctg 1260
cttgaggaga tctggaaggt caacttctact ctctggacc accaaatctt cttcgaccctg 1320
caaggggacg tggctctgca cttggagatt gtccagtggc aatgggaccg gagccagaat 1380
cccttccaga gcgtcgctc ctactacccc ctgcagcgac agctgaagaa catccaagac 1440
atctcctggc acaccgtcaa caacacgac cctatgtcca tgtgttccaa gaggtgccag 1500
tcagggcaaa agaagaagcc tgtgggcac cactctgct gcttcgagt catcgactgc 1560
cttcccggca ccttctcaa ccacactgaa gatgaatatg aatgccaggc ctgcccgaat 1620
aacgagtggc cctaccagag tgagacctcc tgcttcaagc ggcagctggc cttcctggaa 1680
tggcatgagg caccaccat cgtgtggcc ctgctggccg ccctgggctt cctcagcacc 1740
ctggccatcc tgggtgatatt ctggaggcac ttccagacac ccatagtctg ctcggtggg 1800
ggccccatgt gcttctctgat gctgacactg ctgctggtgg catacatggg ggtcccgggtg 1860
tacgtggggc cgcccaaggt ctccacctgc ctctgcgcgc aggcctctt tcccctctgc 1920
ttcacaattt gcatctcctg tategccgtg cgttctttcc agatcgtctg cgccttcaag 1980
atggccagcc gcttcccacg cgcctacagc tactgggtcc gctaccaggg gccctacgtc 2040
tctatggcat ttatcacggc actcaaaatg gtcattgtgg taattggcat gctggccacg 2100
ggcctcagtc ccaccaccg tactgacccc gatgacccca agatcacaat tgtctcctgt 2160
aaccccaact accgcaacag cctgctgttc aacaccagcc tggacctgct gctctcagt 2220
gtgggtttca gcttcgccta catgggcaaa gagctgcca ccaactacaa cgaggccaag 2280
ttcatcacc tcagcatgac cttctatttc acctcatccg tctccctctg caccttcatg 2340
tctgcctaca gcggggtgct ggtcaccatc gtggacctct tgggtactgt gctcaacctc 2400
ctggccatca gcctgggcta cttcggcccc aagtgtaca tgatcctctt ctaccggag 2460
cgcaacacgc ccgcctactt caacagcatg atccagggt acaccatgag gagggactag 2520

```

<210> 24

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Six-His tag

<400> 24

His His His His His His

1

5